Morton's Toe: Prevalence and Inheritance Pattern among Nigerians

Abstract

Background: Anatomical variations have been genetically linked and the difference in the length of the big toe relative to the second toe (Morton's toe) is not an exception; however, its prevalence and inheritance pattern has been a scientific debate. Therefore, this study investigated the prevalence and inheritance pattern of Morton's toe among Nigerians in Rivers State. **Materials and Methods:** A total of 101 families comprising of 101 parents (fathers and mothers) and 135 offspring were conveniently sampled for this study. The observed big toe pattern was described as "L_{BT}" and "S_{BT}" representing big toe longer than the second toe and big toe shorter or equal to the second toe, respectively. The offspring trait was tabulated alongside the parental combination patterns (i.e., when both parents had L_{BT}, both parents S_{BT} and a combination of L_{BT} and S_{BT}). XLSTAT 2012 (version 4.2.2) Chi-square analysis tested the association between sex and Morton's toe. Mendelian Chi-square gene distribution model evaluated the conformance to simple dominance-recessive pattern, while the Hardy–Weinberg (H-W) equation for allele frequency compared the parental allele frequency to that of the offspring. **Results:** L_{BT} (218; 64.7%) was more in the studied population than S_{BT} (119; 35.3%); with males (63; 18.7%) having slightly higher proportion of SBT (Morton's toe) than females (56; 16.6%), which was without sexual preference ($\chi^2 = 0.141$, $P > 0.932$). The test of offspring gene distribution in conformance to Mendelian simple dominant-recessive monohybrid cross had rather weak result. The H-W equation showed a deviation of offspring allele distribution (1:3:2.5 [2:6:5]) from the parents (1:3:2). **Conclusion:** Morton's toe could be said to be genetically linked, however, its inheritance pattern does not conform to the simple dominant-recessive model, but a more complex pattern. It should be noted that the large frequency of a trait in a population does not make it dominant.

Keywords: *Inheritance pattern, Mendelian trait, Morton's toe, Nigerians*

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Introduction

Hereditary determinant of a trait is called a gene.[1] According to Wain *et al*.[2] and Pearson,[3] a gene is an identifiable region of genomic sequence corresponding to a unit of inheritance which is associated with regulatory and other functional sequence regions. In human population, each gene may have many alleles that differ slightly in nucleotide sequence. These alleles (altogether) carry out the normal function of the gene and produce no observable difference in phenotype. Inherited human traits include the ability to roll your tongue or not, attached or unattached earlobes, dimples or freckles, naturally curly or straight hair, widow's peak or straight hairline, color of skin and hair, cleft or smooth chin and so on. However, humans have numerous traits, but some traits are more frequently seen in population such as free-hanging earlobes, ability to roll their tongue, straight hairline, and right-handedness.[4,5] These traits are often expressed in different patterns, which are applicable in clinical and forensic investigations.[1,6]

The toes are the digit of the foot; five toes are present on each human foot. Each consists of three phalanx bones, the proximal, middle, and distal, except for the big toe (*Hallux*). The phalanx bones of the foot join the metatarsal bones at the interphalangeal joints.[7] The big toe also known as hallux, is the first innermost digit of the foot. It only contains two phalanx bones; the proximal and distal. This bone is very important in stability of the foot and maintaining posture.[7]

According to McDonald,[8] the big toe in some individuals are longer than the second toe (here called "L"), while other people have the big toe shorter than the second toe ("S"). This is sometimes said to be

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controlled by one gene with two alleles; with the allele for "S" dominant to the allele for "L." In Sweden, Romanus[9] found the second toe was longest in 2.95% of 8141 men and suggested that the long second toe was dominant with reduced penetrance. In Cleveland Caucasoid, the frequency of the dominant and recessive phenotypes was 24% and 76%, respectively, with no sex influence and the factor for relatively long hallux recessive to the one for relatively long second toe, expressing 100% penetrance.[10] Beers and Clark[11] described a family in which long second toe occurred in 10 persons in three generations. McKusick,[12] was of the opinion that the findings of Beers and Clark[11] were convincing; however, additional information was required to support the claim that Morton's toe is, indeed, a dominant trait. The results of that accumulative research actually supported nothing, as Morton's toe was said to be both dominant and recessive, depending on the source. One reason for the indecisive answer was that Morton's toe, like several other traits, was previously believed to be Mendelian,[8,13] while others believed its inheritance was based on more complex genetic models.[9,10,12] Therefore, there appears to be conflicting belief as to whether this phenomenon is the result of a dominant or recessive gene trait. Therefore, this study was carried out to evaluate the prevalence and inheritance pattern of Morton's toe among Nigerians.

Materials and Methods

Research design

The study was designed as a cross-sectional analytical research involving the observation of the inheritance pattern of the big toe (Morton's foot) among families of Nigerian descent resident in Port Harcourt. The morphological characteristic of a 101 volunteer families were randomly selected without consideration of ethnicity; since the inherited trait is homogeneous. Each family comprised of at least a father, mother, and a child.

Incomplete families that is single parents or no child, complete families but signs of damaged anatomical parts of choice or surgical intervention and families with a history of foreign descent were excluded from the study.

Ethical consideration

Ethical clearance was obtained from the University Ethics Committee of the Post Graduate School, while written informed consents were obtained from the participating families.

Data collection: Morphogenetic details

The relative difference in the big and second toe was determined by physical examination. All morphogenetic traits were observed on site, documented and enter into a data entry sheets. The trait was obtained according to the families and recorded using the below-mentioned modalities.

Big toe length

The foot is placed on a horizontal surface, the big toe length is observed, and the result classified into [Figure 1];
a. Longer (big toe longer than or equal to the second toe)
b. Shorter (big toe shorter than second toe).

Method of data analysis

Excel input: Data arrangement

All inheritance patterns were represented as families in a tabular form with each family trait considered as a single group of traits. Four parental combinations were observed and the offspring grouped from this combination.

Statistical analysis

The data from this excel input were represented in percentage (%) distribution.

Association test – Chi-square analysis was used to evaluate sex-associated influence in the distribution of Morton's toe.

Mendelian Chi-square analysis was applied to determine the closeness of the observed offspring outcome to the expected Mendelian ratio. The expected outcome calculated from the Mendelian assumption of segregation of allele was used to compare the conformance of the observed outcome (family ratio) to that of the Mendelian outcome and inference subsequently drawn from the result.

Hardy–Weinberg distribution method was used to analyze and compares the allele frequency distribution in parents and offspring.

Results

Data were collected from 101 observed families comprised of 337 individuals comprised of 169 (50%) males and 168 (50%) females [Figure 2], made up of 101 fathers (30%), 101 mothers (30%), 68 sons (20.2%), and 67 daughters (19.8%) [Table 1]. Sex-associated difference in the distribution of Morton's toe is presented in Table 2. The distribution of big-toe length with respect to parental combination and the Mendelian Chi-square test for conformance is presented in Tables 3 and 4, respectively. The comparison of the genotypic allele distribution for the big toe length (B) of the parents [Table 5a] and offspring [Table 5b] are compared in Table 6. Notations were assigned to trait at the end of the analysis to connote frequency of gene (pairs of alleles) which are homozygous dominant, heterozygous dominant, and homozygous recessive [Tables 5a, b and 6].

The result from Table 1 indicates that the distribution of long big toe was more in the studied population than short big. Population distribution of longer big toe length (BB) was 64.7% (218) while longer shorter big toe length (bb) was 35.3% (119). One hundred and five (31.2%) males had longer big toe length (L_{BT}) as against 64 (19.0%) males who had shorter big toe length (S_{BT}), while 113 females (33.5%)
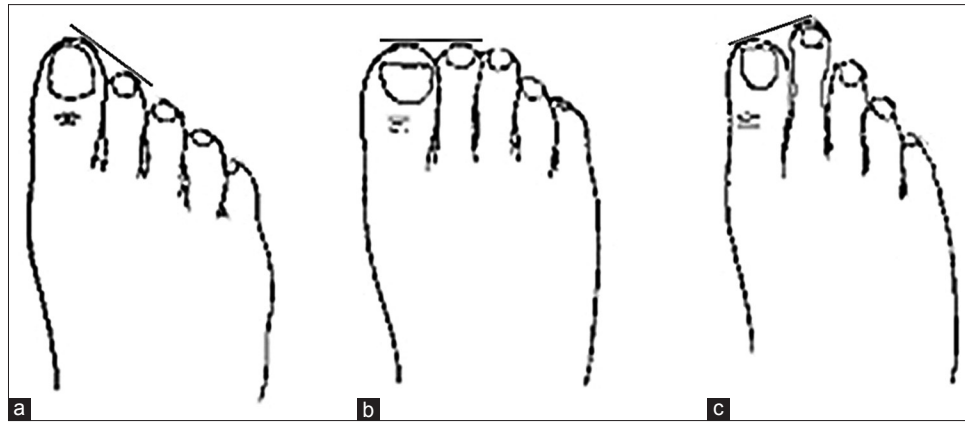
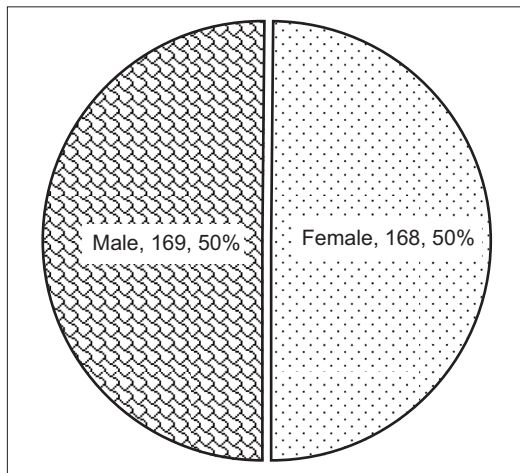Figure 1: (a) and (b) normal or long big toe, (c) Morton's or short big toe

Figure 2: Distribution of the sample population by sex

Table 1: Distribution of big toe length

	Big toe length	
	Long (L$_{BT}$)	Short (S$_{BT}$)
Father		
Count (%)	66 (19.6)	35 (10.4)
Percentage within group	65.30	34.70
Mother		
Count (%)	68 (20.2)	33 (9.8)
Percentage within group	67.30	32.70
Son		
Count (%)	39 (11.6)	29 (8.6)
Percentage within group	57.40	42.60
Daughter		
Count (%)	45 (13.4)	22 (6.5)
Percentage within group	67.20	32.80
Total (%)	218 (64.7)	119 (35.3)

L$_{BT}$: Longer big toe; S$_{BT}$: Shorter big toe

had L$_{BT}$ as against 55 (16.3%) who had S$_{BT}$. No significant association was observed between sex and the morphogenetic trait ($\chi^2_{[df = 1]}$ = 0.013, P = 0.909) [Table 2].

The heterozygous dominant allele constituted 49% of the total allele for the parental big toe length gene [Table 5a]

and 47% of offspring gene [Table 5b]. This produced a genotypic ratio of 1:3:2 for the parents and 1:3:2.5 (2:6:5) for the offspring [Table 6].

Discussion

The study did not observe any bilateral asymmetry (i.e., all individuals displayed uniform foot differences; either both feet had shorter big toe [Morton's toe] or longer big toe), however, the fact that such asymmetry was absent in this study, is not an indication that the authors ruled out the possibility of its existence in the studied population. The frequency of longer big toe (L$_{BT}$; 64.7%) was more when compared to shorter big toe (S$_{BT}$; 35.3%), although the proportion of shorter big toe was higher in the studied population, however, it was in line with the study of Romanus[9] on Swedish adults, which reported 2.95% longer second toe in 8141 men. A higher percentage of males (33.8%) presented with longer big toe than females (30.9%), but the difference was not significant. The observed offspring outcome to the expected outcome in this current study was insignificant when both parental combinations had the same allele combination on the assumption that longer big toe was dominant. This was also noticed for the shorter big toe (Morton's toe); however, significance was observed in the different parental combination when Morton's toe was assumed to be dominant. Hence, longer big toe might have expressed some level of dominance over shorter big toe, but this is not a clear indication of the dominance of the longer big toe. Although various researchers have expressed doubts that Morton's toe, like several other traits such as ear lobe attachment[4,14,15] and nose shape,[5] which is believed to be transmitted in a Mendelian fashion, is rather based on more complex genetic models.[8,13] Kaplan[10] claimed that the relative length of the hallux and second toe is simply inherited with long hallux being recessive; nevertheless, this was not the case in this study; as the Mendelian Chi-square model show more conformance of dominance for the longer big toe.

The equation to determine the contributing allele of a population not only demonstrates the conformance to a

Table 2: Chi-square test of association of sex with the distribution of Morton's toe

	Big toe length		χ^2 analysis				
	L_{BT}	S_{BT}	df	Calculated (χ^2)	Critical (χ^2)	*P*	Inference
Sex (%)							
Male	105 (31.2)	64 (19.0)	1	0.013	3.841	0.909	NS
Female	113 (33.5)	55 (16.3)					
Total	218 (64.7)	119 (35.3)					

NS: Not significant; L_{BT}: Longer big toe; S_{BT}: Shorter big toe

Table 3: The frequency, percentage, and distribution of big-toe length with respect to parental combination

Parents big-toe length combinations	Total number of offspring (%)			Male offspring			Female offspring		
	L_{BT}	S_{BT}	Total	L_{BT}	S_{BT}	Total	L_{BT}	S_{BT}	Total
Long big-toe length in both parents	52 (81)	12 (19)	64 (47)	24	6	30	28	6	34
Expected outcome (if long big-toe length is dominant)	48	16							
Expected outcome (if short big-toe length is dominant)	0	64							
Short big-toe length in both parents	3 (18)	14 (82)	17 (13)	1	8	9	2	6	8
Expected outcome (if long big-toe length is dominant)	0	17							
Expected outcome (if short big-toe length is dominant)	4.25	12.75							
Long in father and short in mother	15 (60)	10 (40)	25 (19)	7	5	12	8	5	13
Expected outcome (if long big-toe length is dominant)	18.75	6.25							
Expected outcome (if short big-toe length is dominant)	6.25	18.75							
Short in father and long in mother	14 (48)	15 (52)	29 (21)	7	10	17	7	5	12
Expected outcome (if long big-toe length is dominant)	14.5	14.5							
Expected outcome (if short big-toe length is dominant)	14.5	14.5							
Total	84 (62)	51 (38)	135	39	29	68	45	22	67

L_{BT}: Longer big toe; S_{BT}: Shorter big toe

Table 4: Mendelian Chi-square test for frequency of big toe length pattern (expected to observed outcome)

Parents big-toe length combinations	If L_{BT} is dominant			If S_{BT} is dominant		
	Calculated	Critical	Inference	Calculated	Critical	Inference
Long big-toe in both parents	1.333	3.841	Insignificant*	2.250	3.841	Insignificant
Short big-toe in both parents	0.529	3.841	Insignificant*	0.123	3.841	Insignificant
Long in father and short in mother	3.000	3.841	Insignificant*	12.250	3.841	Significant
Short in father and long in mother	5.523	3.841	Significant	6.284	3.841	Significant

*More insignificant distributions with lower *P* value observed for long big-toe; therefore, it can be stated that longer big toe expressed dominance over SBT. SBT: Shorter big toe

Table 5a: Parental allele frequency determination for big toe length (B)

Gene	Description	Proportion	Percentage (%)	Total allele
	Total population	202		404
bb	Homozygous short big toe; SBT (q^2)	0.34	34	
b	Allele	0.58		
B	Allele	0.42		
BB	Homozygous long big toe; LBT (p^2)	0.18	18	
Bb	Heterozygous long big toe; LBT ($2pq$)	0.49	49*	
				Ratio=BB : Bb : bb
				0.18 : 0.49 : 0.34-1:3:2
Total population				**Long big toe**
Actual number of homozygous L_{BT}				36
Actual number of heterozygous L_{BT}				98*
Total				134

BB: Homozygous for long big toe; Bb: Heterozygous form for long big toe; bb: Homozygous short big toe; S_{BT}: Shorter big toe; *Highest contributing allelic form

Table 5b: Offspring allele frequency determination for big toe length (B)

Gene	Description	Proportion	Percentage (%)	Total allele
	Total population	135		270
bb	Homozygous short big toe; SBT (q^2)	0.38	38	
b	allele	0.61		
B	allele	0.39		
BB	Homozygous long big toe; LBT (p^2)	0.15	15	
Bb	Heterozygous long big toe; LBT (2pq)	0.47	47*	Ratio=BB : Bb : bb
				0.15 : 0.47 : 0.38-1:3:2.5

Total population	Long big toe
Actual number of homozygous LBT	20
Actual number of heterozygous LBT	64
Total	84*

BB: Homozygous for long big toe; Bb: Heterozygous form for long big toe; bb: Homozygous short big toe; S_{BT}: Shorter big toe; *Highest contributing allelic form

Table 6: Summary of genotypic ratio of the various traits

Ratio	Big toe length BB:Bb:bb
Parental genotype (ratio)	1:3:2
Offspring genotype (ratio)	1:3:2.5 (2:6:5)*

*Nonconformance to parental distribution

nonevolving population with a phenotypic ratio of 3:1, and genotypic ratio of 1:2:1, but additionally for examining the genotypic and phenotypic ratios of both parents and offspring. This was clearly demonstrated and understood during the Mendelian experiment (with a perfect Chi-square values [$\chi^2 = 1$ and $P = 0.00$]), which was attributed to the fact that controlled breeding (pure breeding) was achieved in the test population, but such cannot be achieved in a naturally occurring human population. However, it will be noteworthy to emphasize that the genetic makeup of the offspring was expected to be a representation of the parent; but a marked deviation from the parental ratio of 1:3:2 (BB: Bb: bb) was observed, as the offspring exhibited higher "bb" (2:6:5; BB:Bb:bb). This outcome could be attributed to the indifference during the Mendelian Chi-square test that produced insignificance for both L_{BT} (BB; Bb) and S_{BT} (bb) when both parents expressed either of the combination. In addition, when the heterozygous allele and homozygous recessive allele are of higher percentage, they tend to favor the appearance of homozygous recessive traits; which was evident from the calculations; as the homozygous recessive allele in parent (0.58%) increased in the offspring (0.61%).

The claims of McDonald,[8] Romanus,[9] Kaplan,[10] and Morton[13] on the inheritability of Morton's toe is very well agreed, however, the pattern of inheritance cannot be scientifically stated to be in a simple Mendelian fashion, as this study observed an insignificance value for both the short and long big toe in the offspring to the Mendelian value ($\chi^2 = 3.841$) when both parents displayed same pattern (short; S_{BT} and long; L_{BT}). In addition, the genotypic ratio of Morton's toe in the offspring did not follow the same ratio as the parents, thus suggesting that it exhibit a more complex inheritance pattern as described by Morton[13] and McDonald.[8]

Conclusion

The pattern of inheritance of Morton's toe was without sex predisposition, with larger population exhibiting longer big toe. Undoubtedly, Morton's toe is genetically inherited, but deviation from the Mendelian model was evident that its inheritance does not conform to the simple dominant-recessive fashion. It must be noted that the appearance of large frequencies of a trait in a population does not make it dominant.

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Conflicts of interest

There are no conflicts of interest.

References

1. Daniel LH, Elizabeth WJ. Genetics: Principles and Analysis. 4th ed. Canada: Jones and Bartlett Publishers; 1998. p. 31-52, 60-71, 668-75.
2. Wain HM, Bruford EA, Lovering RC, Lush MJ, Wright MW, Povey S, *et al*. Guidelines for human gene nomenclature. Genomics 2002;79:464-70.
3. Pearson H. Genetics: What is a gene? Nature 2006;441:398-401.
4. Ordu KS Didia BC, Egbunefu N. Inheritance pattern of earlobe attachment amongst Nigerians. Greener J Med Sci 2014;2:1-7.
5. Ordu SK, Aigbogun EO Jr., Nwankwo JC. Evaluation of nose shape as a mendelian inherited trait in the determination of parentage among Nigerians in Port Harcourt. J Exp Clin Anat 2016;15:9-13.
6. Miko I, LeJeune L, editors. Essentials of Genetics. Cambridge, MA: NPG Education; 2009. p. 43-9.
7. Moore KL, Dailey AF. Upper limb. Clinically Oriented Anatomy. 3rd ed. Baltimore: Lippincott Williams & Wilkins; 2006. p. 679-80.
8. McDonald JH. Hitchhiker's thumb. Myths of Human Genetics. USA, Maryland: Sparky House Publishing Baltimore; 2011. p. 49-50.

9. Romanus T. Heredity of a long second toe. Hereditas 1949;35:651-2.
10. Kaplan AR. Genetics of relative toe lengths. Acta Genet Med Gemellol (Roma) 1964;13:295-304.
11. Beers CW, Clark LA. Tumors and the short toe – A dihybrid pedigree. J Hered 1942;33:336.
12. McKusick VA. Mendelian inheritance in man. A Catalog of Human Genes and Genetic Disorders. 12th ed. Baltimore: Johns Hopkins University Press; 1998.
13. Morton DJ. Inheritance of a long second toe. J Hered 1952;43:49-50.
14. Hilden K. Uber die from des ohlappchensbeim menschen und ihre abhangigkeit von erblanglagen. Hereditas 1922;3:351-7.
15. Powell FF, Whitney DD. Earlobe inheritance: An unusual three generation photo graphic pedigree chart. J Hered 1937;28:184-6.